



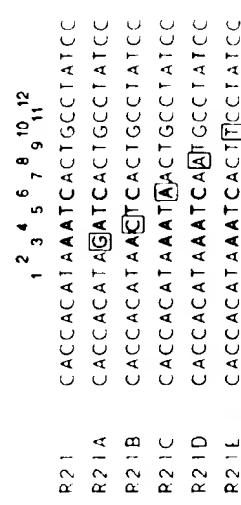
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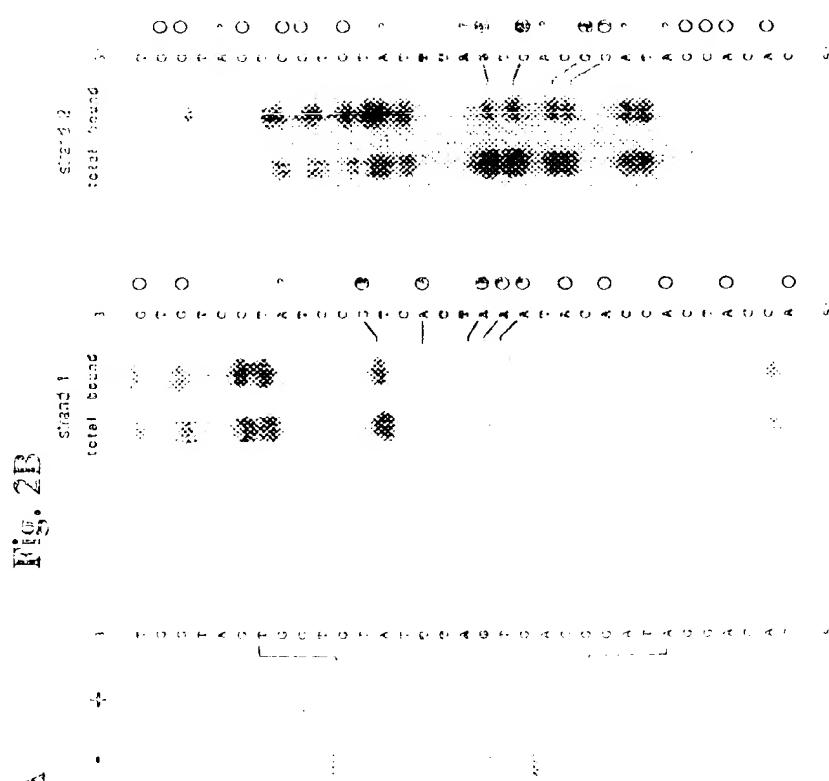
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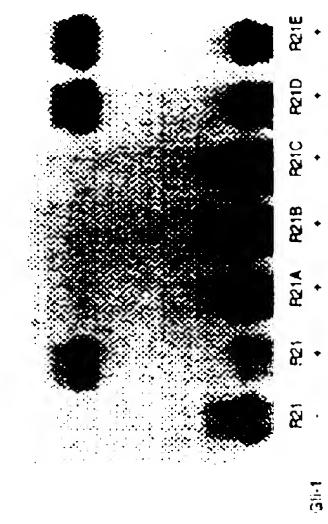


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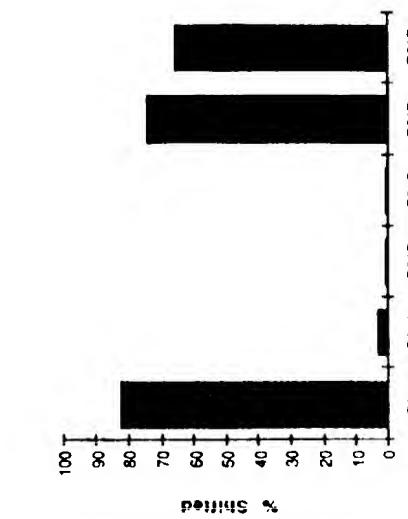


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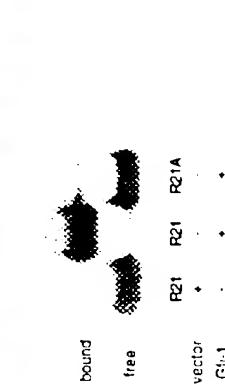
10<sup>10</sup>–10<sup>12</sup>



2D3



2E



**SUBSTITUTE SHEET (RULE 26)**

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Fig. 3A HCMV MIE Promoter

GCCTGCTGGCTGACCGCCAAACGACCCCCGCCCATTGACGTCAATAATG  
ACGTATGTTCCCATAGTAACGCCAAATAGGACTTTCATTGACGTCAATG  
GGTGAGTAACTTACCGTAAACTGCCCACTTGGCAAGTACATCAAGTGTATC  
ATATGCCAAAGTACGCCCTATGACGTCAATGACGGTAAATGGCCGCC  
TGGCATATATGCCAGTACATGACCTTATGGGACTTCCCTACTTGGCAGTA  
CATCTACGTATTAGTCATCGCTATTACCATGGTGTGATGGGTTTGGCAGT  
ACATCAATGGCGTTGATAGCGGTTTGACTGACCTGGGATTTTGTAAAGTC

Fig. 3C Point Mutations

	Gli-1 site #1	Gli-1 site #2
Wildtype CMV	CACGGG <u>GAA</u> TTTC	.....AAA <u>AATCA</u> ACGGG
Mutant A	CACGGG <u>GAT</u> TTTC	.....AAA <u>GTC</u> AACGGG
Mutant B	CACGGG <u>GAC</u> TTTC	.....AAA <u>ACT</u> AACGGG

Fig. 3D

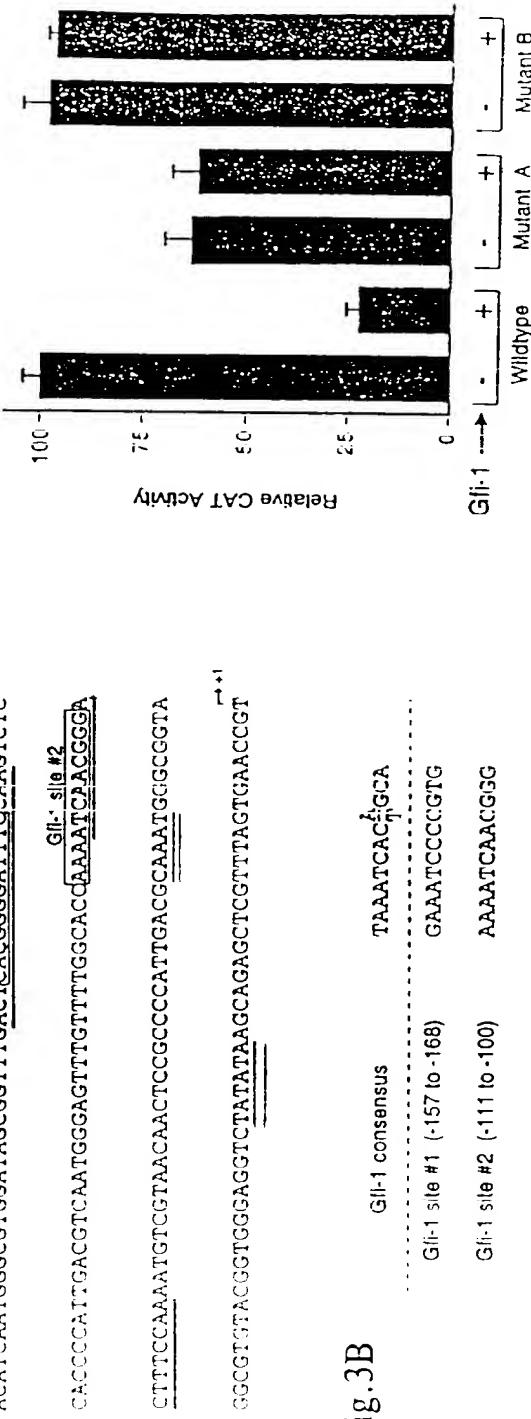


Fig. 3B

Gli-1 consensus	TAATCAC <u>G</u> CA
Gli-1 site #1 (-157 to -168)	GAATCCCCGTG
Gli-1 site #2 (-111 to -100)	AAA <u>ATCAACGGG</u>

Fig. 4A

GII-1	Predicted	Binding Site			B21
		3'	5'	6'	
T	-	-	-	-	
G	X	-	-	-	
V	T/C	G	-	-	
H	S	A	C	C	
O	R	G/t	G	C	
Finger 1	D	T	A	T	
Finger 2	K	T	C	A	
Finger 3	N	A	G	T	
Finger 4	T	A	T	A	
Finger 5	R	A	A	T	
Finger 6	D	G/t	T	A	
	R	C	-	-	
	G/t	G/t	T	A	
	D	C	-	-	
	R	G/t	G/t	G/t	
		5'	6'	3'	

Fig. 4B

